

**Human protein: Q8TBE1 - Cornichon-like protein. - EMBL Bioinformatic Harvester**EMBL-Heidelberg - [harvester \(c\)](#) - [technology](#) - [gfp-cdna](#) - [pepperkok-team](#) - [contact](#) -Length: **160 aa**, molecular weight: **18976 Da**, CRC64 checksum: **CF7E8645A9587504**

MAFTFAAF	FCY	MLSLVL	CAAL	IFFAIW	HIIA	FDELRT	DFKS	PIDQCN	PVHA	RERLRN	IERI	60		
CFLLRK	LVL	PEYSI	HS	LF	CI	MFLCA	QEWLT	LGLNV	PLLFY	HFWR	YFHCPA	DSSE	LAYDPP	120
VVMNAD	TL	SY	CQKEA	WCKLA	FYLLS	FFYYL	YCM	IY	TL	VSS				160

//

GoTo: EBI - Hinxton - "SWALL" database**General information**Entry name **CNIL\_HUMAN**Accession number **Q8TBE1**

Created Rel. 41, 28-FEB-2003

Sequence update Rel. 41, 28-FEB-2003

Annotation update Rel. 42, 15-SEP-2003

**Description and origin of the Protein**

Description Cornichon-like protein.

Gene name(s) CNIL.

Organism source Homo sapiens (Human).

Taxonomy Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI TaxID 22388257

PubMed AK096312;[BAC04760.1](#);.[BC022780](#);[AAH22780.1](#);.

InterPro PF03311;Cornichon;1.

PROSITE Transmembrane;

**Features**

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Key	Begin	End	Length	Description
<u>TRANSMEM</u>	11	31	21	POTENTIAL.
<u>TRANSMEM</u>	73	93	21	POTENTIAL.
<u>TRANSMEM</u>	139	159	21	POTENTIAL.

## Activate BLAST of: Q8TBE1

	BLAST	Pro
	Genome	Nucle

Query: gi|21755779 hypothetical protein FLJ38993 [Homo sapiens]

Matching gi: 18490801, 26329545, 27805431, 22749039

Best hits

Common Tree

Taxonomy Report

3D structures

CDD-Search

Gelis

31 BLAST hits to 12 unique species Sort by taxonomy proximity☐

Archaea

☐

Bacteria

☒

Metazoa

☒

Fungi

☒

Plants

☐

Viruses
























☐

Other Eukaryotae

Keep only

Cut-Off

160 aa

	SCORE	P	ACCESSION	GI	PROTEIN DESCRIPTION
	847	21	BAB28996	12851288	unnamed protein product [Mu
	729	21	BAA21746	4521254	cornichon-like protein [Mus
	578	21	AAC15828	2460430	cornichon [Mus musculus]
	577	27	AAC98388	4063709	cornichon [Homo sapiens]
	521	27	AAD32301	4894209	cornichon-like protein [Hom
	499	10	AAK15762	13195570	cornichon [Boltenia villosa
	403	8	AAA86527	886769	cni gene product
	401	8	P52159	1705957	CORNICHON PROTEIN
	390	8	EAA14788	30174276	ENSANGP00000019460 [Anophel
	389	7	CAB01516	5824608	Hypothetical protein T09E8.
	359	27	CAD62612	28207917	unnamed protein product [Ho
	355	7	A89261	25336821	protein T09E8.3 [imported]
	207	21	BAB32366	12862150	unnamed protein product [Mu
	205	27	AAF29127	6841548	HSPC163 [Homo sapiens]
	203	21	XP_213960	27679416	similar to RIKEN cDNA D5300
	176	21	XP_136930	20853677	similar to cornichon homolo
	174	4	EAA30033	28920672	hypothetical protein [Neuro
	159	4	CAA96756	1322550	ORF YGL054c [Saccharomyces
	156	4	CAB90792	7768496	putative er-derived vesicle
	154	8	EAA14707	21302562	ENSANGP00000010644 [Anophel
	154	8	AAF51153	7295853	CG17262-PA [Drosophila mela
	152	7	AAK39349	13775541	Hypothetical protein Y64H9A
	128	4	CAB16265	2414616	unnamed protein product

S.O.U.R.C.E.  
SearchGeneReport for:  
AK096312

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SOURCE  
GeneReport  
187 sequences

# FLJ38993

## hypothetical protein FLJ38993

[UniGene](#), [LocusLink](#), [OMIM](#), [GenAtlas](#), [GeneCard](#), [Ensembl](#), [MapView](#), [Genome Browser](#)

### Chromosomal Location

**Chromosome/Cytoband** 1q42.12

### Annotations

Gene Ontologies	Ontology	Annotation	Evidence	Sour
	Biological Process	Intracellular signaling cascade	IEA	GOA
	Cellular Component	Integral to membrane	IEA	GOA

### UniGene & EST Expression Information

#### UniGene Cluster

**Hs.13410 from Build No. 160** , Released on 2003-03-29

Normalized expression  
distribution for tissue  
type  
Top ten [of 13]

[[Help](#)]

Tissue	Normalized Expression (%)	Cluster Clones : Tissue clon
malignant melanoma, metastatic to lymph node:	22.22	1:2723
testis:	11.62	1:5207
total brain:	11.57	2:10454
large cell carcinoma, undifferentiated:	10.73	1:5637
melanotic melanoma:	10.36	10:58397
glioblastoma with EGFR amplification:	7.25	1:8343
medulla:	6.60	1:9172
hippocampus:	6.52	2:18566
melanotic melanoma, high MDR (cell line):	5.91	1:10228
melanotic melanoma, cell line:	3.34	1:18104

#### SAGE (NCBI)

Go to [Gene-to-tag Mapping](#) at NCBI

### Upstream Genomic Sequence

#### TRASER

[Upstream genomic sequence](#) for hypothetical protein FLJ38993

### Representative mRNA Sequences

#### UniGene

**NM\_152495**

#### LocusLink RefSeq

Accession	Description
NM_152495	NA

### Alias PubMed Search

[PubMed](#)[Search PubMed using aliases AND](#)[PubMed](#)[Search](#)[No Clone Report](#)[Help](#)[ACTIVATE: SMART analysis](#)

name	begin	end	E-value
Pfam:Cornichon	6	152	1.20e-68

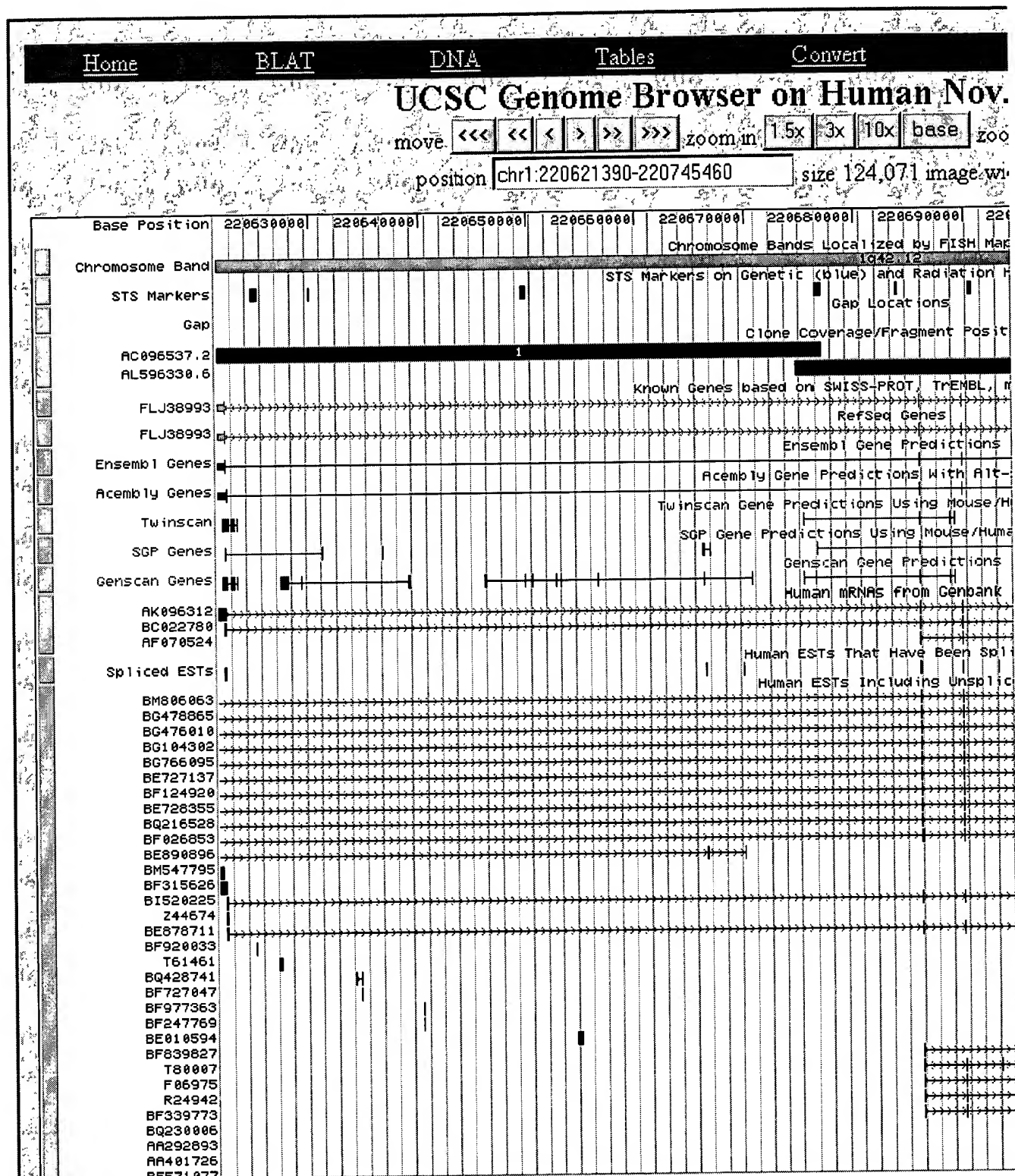
These features and domains are not shown in the diagram, either because their scores are less significant than the required threshold, or because they overlap with some other source of annotation:

name	begin	end	E-value	reason
<a href="#">signal peptide</a>	1	18	-	overlap
<a href="#">transmembrane</a>	7	29	-	overlap
<a href="#">transmembrane</a>	77	99	-	overlap
<a href="#">transmembrane</a>	139	158	-	overlap
<a href="#">low complexity</a>	139	151	-	overlap

Summary of BLAST results. Note that the probabilities are not directly comparable to those in the table above.

name	seq	begin	end	E-value
<a href="#">SCOP:d1erza</a>	<a href="#">d1erza</a>		44	5.30e+00
<a href="#">SCOP:d1eija</a>	<a href="#">d1eija</a>	50	71	3.10e+00

[Activate IPsort of: Q8TBE1](#)[Activate Genome Browser of: Q8TBE1](#)



[Activate MapView of: Q8TBE1](#)

NCBI  
PubMed Entrez BLAST OMIM

Search  Find in This View

**Homo sapiens Map View build 33** **BLAST the Human Genome**

Chromosome: [ 1 ] 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X Y

Query: AK096312>all matches [clear]

Master Map: Genes On Sequence **Maps & Options**

Total Genes On Chromosome: 3232 [153 not localized]  
Region Displayed: 215M-222M bp [Download/View Sequence/Evidence](#)  
Genes Labeled: 20 Total Genes in Region: 84

Gene...	HsUniG	Genes_seq	symbol	links
		216M	DKFZp547M236	+ <a href="#">sv</a> <a href="#">ev</a> - <a href="#">seq</a> <a href="#">mr</a>
			RAB3-GAP150	+ <a href="#">sv</a> <a href="#">ev</a> - <a href="#">seq</a> <a href="#">mr</a>
		217M	FLJ14146	+ <a href="#">sv</a> <a href="#">ev</a> - <a href="#">seq</a> <a href="#">mr</a>
			FLJ20605	+ <a href="#">sv</a> <a href="#">ev</a> - <a href="#">seq</a> <a href="#">mr</a>
			DUSP10	+ <a href="#">sv</a> <a href="#">ev</a> <a href="#">hm</a> <a href="#">seq</a> <a href="#">m</a>
		218M	FLJ13840	+ <a href="#">sv</a> <a href="#">ev</a> <a href="#">hm</a> <a href="#">seq</a> <a href="#">m</a>
			DISPA	+ <a href="#">sv</a> <a href="#">ev</a> <a href="#">hm</a> <a href="#">seq</a> <a href="#">m</a>
			FLJ35728	+ <a href="#">sv</a> <a href="#">ev</a> - <a href="#">seq</a> <a href="#">mr</a>
		219M	CAPN2	+ <a href="#">sv</a> <a href="#">ev</a> <a href="#">hm</a> <a href="#">seq</a> <a href="#">m</a>
			TP53BP2	+ <a href="#">sv</a> <a href="#">ev</a> - <a href="#">seq</a> <a href="#">mr</a>
			FLJ38993	+ <a href="#">sv</a> <a href="#">ev</a> - <a href="#">seq</a> <a href="#">mr</a>
		220M	LBR	+ <a href="#">sv</a> <a href="#">ev</a> - <a href="#">seq</a> <a href="#">mr</a>
			PRO0650	+ <a href="#">sv</a> <a href="#">ev</a> - <a href="#">seq</a> <a href="#">mr</a>
			EPHX1	+ <a href="#">sv</a> <a href="#">ev</a> <a href="#">hm</a> <a href="#">seq</a> <a href="#">m</a>
		221M	KIAA0792	+ <a href="#">sv</a> <a href="#">ev</a> - <a href="#">seq</a> <a href="#">mr</a>
			LEFTB	+ <a href="#">sv</a> <a href="#">ev</a> <a href="#">hm</a> <a href="#">seq</a> <a href="#">m</a>
			EBAF	+ <a href="#">sv</a> <a href="#">ev</a> <a href="#">hm</a> <a href="#">seq</a> <a href="#">m</a>
		222M	FLJ35382	+ <a href="#">sv</a> <a href="#">ev</a> - <a href="#">seq</a> <a href="#">mr</a>
			GOCAP1	+ <a href="#">sv</a> <a href="#">ev</a> - <a href="#">seq</a> <a href="#">mr</a>
			MIXL1	+ <a href="#">sv</a> <a href="#">ev</a> - <a href="#">seq</a> <a href="#">mr</a>

Region Shown: 215981389 222838203

out 200M in

ideogram master

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Activate: STRING of: Q8TBE1

[Home](#)[Download](#)[Help/Info](#)**STRING****No predictions found ...**

Sorry, we have not found any functional associations in our database.

Your input was 'Q8TBE1' (Similar to RIKEN cDNA 2900075G08 gene).

This gene is not a member of an orthologous group, which is a prerequisite for genomic context methods.

Please note that STRING works best for prokaryotes, although it contains many predictions for eukaryotes as well - mainly in the areas metabolism and information processing.

Orthology information is derived from the COG database, which we extended to cover more species and more genes, using an automatic update mechanism.

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Activate: Conserved Domains of: Q8TBE1



**ACTIVATE: SOSUI analysis**

This amino acid sequence is of a MEMBRANE PROTEIN  
which have 3 transmembrane helices.

No.	N terminal	transmembrane region	C terminal	type	length
1	7	AFCYMLSLVLCAALIFFAIWHII	29	PRIMARY	23
2	81	MFLCAQEWLTLGLNVPLLFYHFW	103	SECONDARY	23
3	136	WCKLAFYLLSFFYYLYCMIYTLV	158	PRIMARY	23

**ACTIVATE: IPSORT analysis****iPSORT Prediction**

**Predicted as: *having a signal peptide***

Sequence (Type: nonplant)

1 MAFTF AAFCY MSLSV LCAAL IFFAI WHIIA FDEL R TDFKS PIDQC NPVHA  
51 RERLR NIERI CFLLR KLVLP EYSIH SLFCI MFLCA QEWT LGLNV PLLFY  
101 HFWRY FHCPA DSSEL AYDPP VMNA DTLSY CQKEA WCKLA FYLLS FFYYL  
151 YCMIY TLVSS

**Values used for reasoning**

Node	Answer	View	Substring	Value(s)	Plot
1. Signal peptide?	Yes	Average Hydropathy (KYTJ820101)	[6,20]	2.28 ( $\geq 0.953$ ? Yes)	<a href="#">show</a>
2. Mitochondrial ?	No	Average Net Charge (KLEP840101)	[1,30]	0 ( $\geq 0.083$ ? No)	<a href="#">show</a>
		Indexing: All Pattern: 221121122 (ins/del $\leq 3$ )	[1,30]	MAFTFAAFCYMLSLVLCAA--L-IFFAIWHIIA 22222222222222222222--2-1222120112 221121122	--

\* This color means "not used".

Name	Alphabet Indexing		
	0	1	2



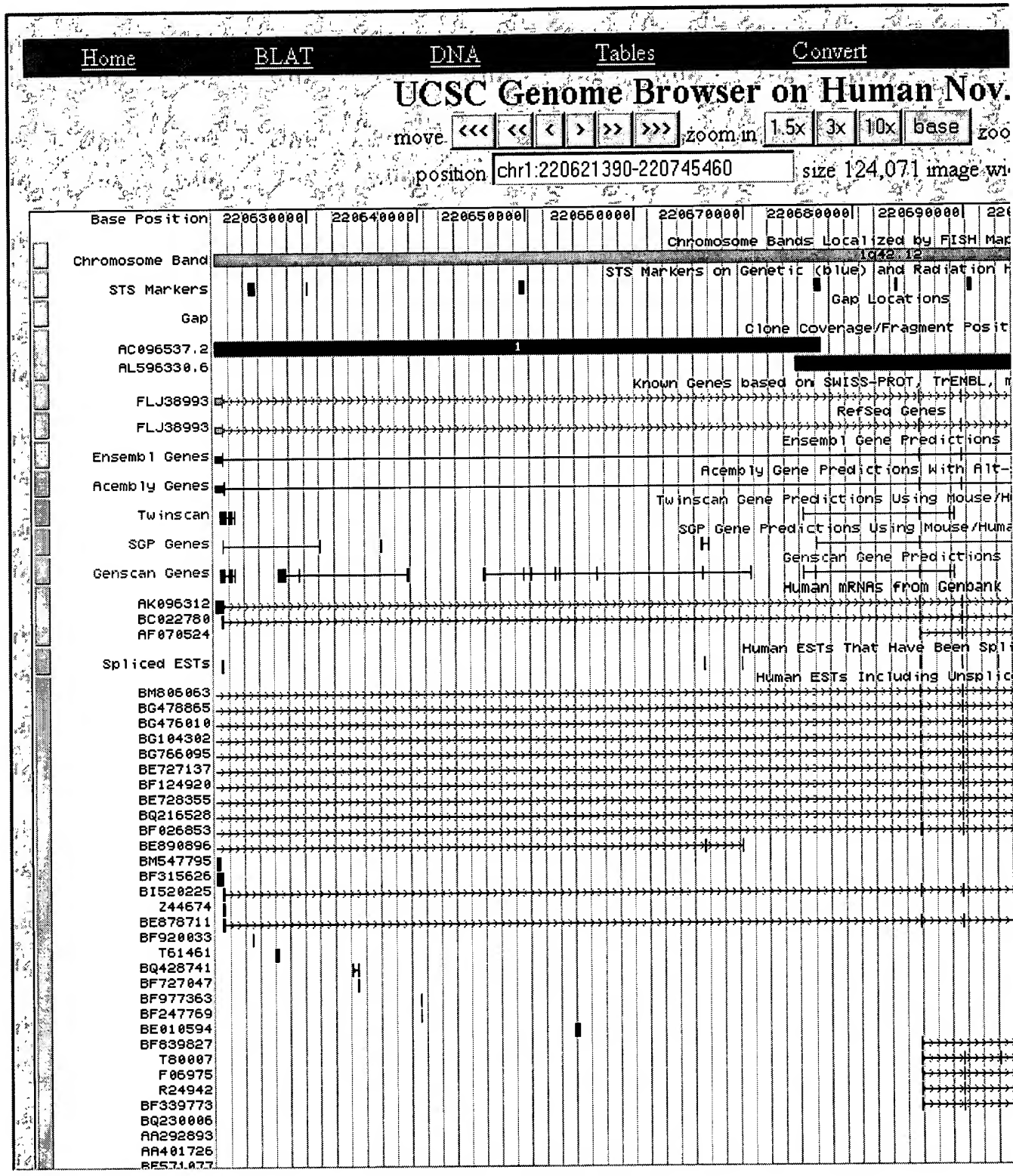
<b>AI1</b>	DEGHKN	<b>IR</b>	ACFLMPQSTVWY
<b>AI2</b>	ACDEFGHLMNQSTVWY	<b>KR</b>	IP

[Return to iPSORT Home](#)

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[Activate Genome Browser of: Q8TBE1](#)



[Activate MapView of: Q8TBE1](#)

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PubMed Entrez BLAST OMIM

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MapView Home  
Map Viewer Help  
Human Maps Help  
FTP

Data As Table View  
**Maps & Options**  
Compress Map ☒

Region Shown:

☒ out  
☒ 200M  
☒ in

☒ ideogram  
☒ master

**Homo sapiens Map View build 33** **BLAST the Human Genome**

Chromosome: [1](#) [2](#) [3](#) [4](#) [5](#) [6](#) [7](#) [8](#) [9](#) [10](#) [11](#) [12](#) [13](#) [14](#) [15](#) [16](#) [17](#) [18](#) [19](#) [20](#)  
[21](#) [22](#) [X](#) [Y](#)

Query: AK096312>all matches

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			RAB3-GAP150	↑ <a href="#">sv</a> <a href="#">ev</a> - <a href="#">seq</a> <a href="#">mrr</a>
		217M	FLJ14146	↑ <a href="#">sv</a> <a href="#">ev</a> - <a href="#">seq</a> <a href="#">mrr</a>
			FLJ20605	↑ <a href="#">sv</a> <a href="#">ev</a> - <a href="#">seq</a> <a href="#">mrr</a>
			DUSP10	↑ <a href="#">sv</a> <a href="#">ev</a> <a href="#">hm</a> <a href="#">seq</a> <a href="#">m</a>
		218M	FLJ13840	↑ <a href="#">sv</a> <a href="#">ev</a> <a href="#">hm</a> <a href="#">seq</a> <a href="#">m</a>
			DISPA	↓ <a href="#">sv</a> <a href="#">ev</a> <a href="#">hm</a> <a href="#">seq</a> <a href="#">m</a>
			FLJ35728	↓ <a href="#">sv</a> <a href="#">ev</a> - <a href="#">seq</a> <a href="#">mrr</a>
		219M	CAPN2	↑ <a href="#">sv</a> <a href="#">ev</a> <a href="#">hm</a> <a href="#">seq</a> <a href="#">m</a>
			TP53BP2	↑ <a href="#">sv</a> <a href="#">ev</a> - <a href="#">seq</a> <a href="#">mrr</a>
			FLJ38993	↓ <a href="#">sv</a> <a href="#">ev</a> - <a href="#">seq</a> <a href="#">mrr</a>
		220M	LBR	↑ <a href="#">sv</a> <a href="#">ev</a> - <a href="#">seq</a> <a href="#">mrr</a>
			PRO0650	↓ <a href="#">sv</a> <a href="#">ev</a> - <a href="#">seq</a> <a href="#">mrr</a>
			EPHX1	↓ <a href="#">sv</a> <a href="#">ev</a> <a href="#">hm</a> <a href="#">seq</a> <a href="#">m</a>
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			LEFTB	↑ <a href="#">sv</a> <a href="#">ev</a> <a href="#">hm</a> <a href="#">seq</a> <a href="#">m</a>
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		222M	FLJ35382	↑ <a href="#">sv</a> <a href="#">ev</a> - <a href="#">seq</a> <a href="#">mrr</a>
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			MIXL1	↓ <a href="#">sv</a> <a href="#">ev</a> - <a href="#">seq</a> <a href="#">mrr</a>

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[Activate CDART of:Q8TBE1](#)**CDART: Conserved Domain Architecture Retrieval To**[New Query](#)[Overview](#)[PubMed](#)[Nucleotide](#)[Protein](#)[Structure](#)[Taxonomy](#)

Query

[more>](#)**Similar domain architectures**

35 Sequences

Eukaryota

Cornichon-like pro



AAF79631

Arabidopsis thaliana

F5011.7

[more>](#)Result page: [Previous](#) 1 [Next](#)**Subset**

by Taxonomy

**Subset**

by selected domains:

[pfam03311](#)

Cornichon protein.

[pfam04127](#)

DNA / pantothenate metabolism flavoprotein. The D...

includes:

[COG0163](#) [COG0452](#) [COG1036](#) [pfam02441](#)[Help](#) | [Disclaimer](#) | [Write to the Help Desk](#)[NCBI](#) | [NLM](#) | [NIH](#)

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Activate SOSUI of:Q8TBE1

## SOSUI Result

Query title :

Total length : 160 A. A.

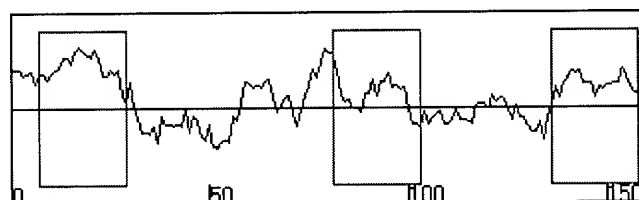
Average of hydrophobicity : 0.600000

**This amino acid sequence is of a MEMBRANE PROTEIN  
which have 3 transmembrane helices.**

No.	N terminal	transmembrane region	C terminal	type	length
1	7	AFCYMLSLVLCAALIFFAIWHII	29	PRIMARY	23
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3	136	WCKLAFYLLSFFYYLYCMIYTLV	158	PRIMARY	23

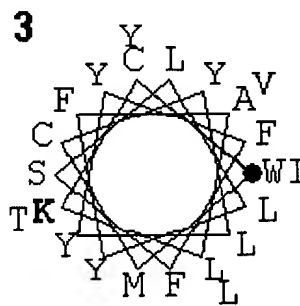
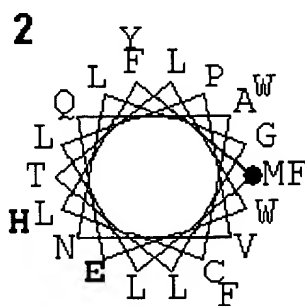
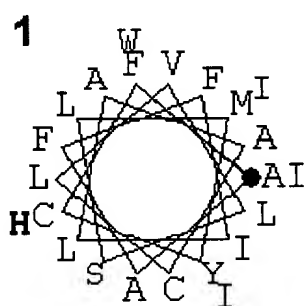
## Display Options

### [Hydropathy profile]



### [Helical wheel diagram of predicted segments]

Hydrophobic residue: Black  
Polar residue: Blue  
Charged residue: Bold blue(+) Bold red(-)




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Activate: STRING of: Q8TBE1

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